

In the Specification:

Please replace the paragraph beginning at page 20, line 24, with the following:

--Selection of Peptides: The entire amino acid sequence of equine IgE, based on the predicted 566 translated amino acids, was used to generate algorithms to predict accessible epitopes. The algorithms combine the Hopp and Woods hydrophilicity scale, surface probability and accessibility scales, Karplus and Schulz flexibility scale, and Jameson-Wolf antigenic index. Chou and Fasman algorithms were used to determine secondary structure including turns, alpha helices, and beta sheets. Based on data obtained from the above algorithms, six 15 amino acid length peptides were selected for synthesis. The following is a list of the chosen peptides and their location on the epsilon heavy chain: P1 (VTYKRHDLLRTRPRK; SEQ ID NO:1) end portion of C2, P2 (RTRPRKCTESEPRGV; SEQ ID NO:2) end portion of C2, P3 (LAACCKDTKTTNITL; SEQ ID NO:3) beginning of C1, P4 (IQTDQQATTRPKSQW; SEQ ID NO:4) early portion of C4, P5 (LIDGQKVDEQFPQHG; SEQ ID NO:5) middle portion of C2, P6 (RVVASGKWAKQKFTC; SEQ ID NO:6) latter portion of C1. All peptides were manufactured by Sigma Genosys, purified by HPLC, and provided as lyophilized powder.--

Please insert the accompanying paper copy of the Sequence Listing, page numbers 1 to 2, at the end of the application.

REMARKS

Applicants request entry of this amendment in adherence with 37 C.F.R. §§1.821 to 1.825. This amendment is accompanied by a floppy disk containing the above named sequences, SEQ ID NOS:1-6, in computer readable form, and a paper copy of the sequence information which has been printed from the floppy disk.